

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/770,643A

DATE: 09/10/2001  
TIME: 08:33:19

Input Set : A:\LEX-0122-USA SEQLIST.txt  
Output Set: N:\CRF3\09102001\I770643A.raw

RECEIVED  
NOV 13 2001  
TECH CENTER 1600/2900

ENTERED

4 <110> APPLICANT: Turner, C. Alexander Jr.  
5 Hilbun, Erin  
6 Donoho, Gregory  
7 Scoville, John  
8 Wattler, Frank  
9 Friedrich, Glenn  
10 Abuin, Alejandro  
11 Zambrowicz, Brian  
12 Sands, Arthur T.  
14 <120> TITLE OF INVENTION: Novel Human Neurexin-like Proteins and Polynucleotides  
Encoding the  
15 Same  
17 <130> FILE REFERENCE: LEX-0166-PRV  
C--> 19 <140> CURRENT APPLICATION NUMBER: US/09/770,643A  
C--> 19 <141> CURRENT FILING DATE: 2001-01-26  
19 <160> NUMBER OF SEQ ID NOS: 31  
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
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24 <211> LENGTH: 3924  
25 <212> TYPE: DNA  
26 <213> ORGANISM: homo sapiens  
28 <400> SEQUENCE: 1  
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31 atggcttttt ccagttcctc agacctcact ggcactcaca gcccagctca actcaactgg 180  
32 agagttggaa ctggcggttg gtccccagca gattccaatg ctcaacagtg gctccagatg 240  
33 gacctgggaa acagagtaga gattacagca gtggccacgc aggaagata cggaagctct 300  
34 gactgggtga cgagttacag cctgatgttc agtgacacag gacgcaactg gaaacagtac 360  
35 aaacaagaag acagactctg gacctttgca ggaacatga atgctgacag cgtgggtcac 420  
36 cacaagctat tgcactcagt gagagcccgat tttgttcgct ttgtgcccct ggaatggaat 480  
37 cccagtggga agattggcat gagagtcgag gtctacggat gttcctataa atcagacggt 540  
38 gctgactttg atggccgaag ctactttctg tacaggttca atcagaagtt gatgagtact 600  
39 ctcaaagatg tgatctccct gaagttcaag agcatgcaag gagatggggt cctgttccat 660  
40 ggagaagggt agcgtggaga ccacatcacc ttggaactcc agaaggggag gctcgcccta 720  
41 cacctcaatt tgggtgacag caaagcgagg ctacagcaga gcttgccctc tgccaccctg 780  
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43 gtgaacttca cggtggacaa gcacacacag cacttccgca ccaagggcga gacggatgcc 900  
44 ttagacattg actatgagct tagttttgga ggaattccag taccaggaaa acctgggacc 960  
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46 attracctgg ctaagagacg aaagcatcag atctatactg tgggcaatgt cactttttcc 1080  
47 tgetccgaac cacagattgt gcccatcaca tttgtyaact ccagcggcag ctatttctctg 1140  
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50 ctggaggggt gaactctgag actcgtgatt cagaaaatga cagaacgcgt agctgaaatc 1320  
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54 tcccaatggt taaatcccat taaggcttcc caaggctgca tgaggctcat ctttattgat 1560

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61 acccgagtgc ggggcgctaa ccctgagaag ccctatgcca tggccttgga ctacgggggc 1980
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91 atcggagggg tgatagcagt ggtgatattc atcatcttct gtatcatcgg catcatgacc 3780
92 cggttcctct accagcacia gcagtcacat cgtacgagcc agatgaagga gaaggaaat 3840
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96 <210> SEQ ID NO: 2
97 <211> LENGTH: 1307
98 <212> TYPE: PRT
99 <213> ORGANISM: homo sapiens
101 <220> FEATURE:
102 <221> NAME/KEY: VARIANT
103 <222> LOCATION: (1)...(1307)
104 <223> OTHER INFORMATION: Xaa = Any Amino Acid
106 <400> SEQUENCE: 2

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```

107 Met Asp Ser Leu Pro Arg Leu Thr Ser Val Leu Thr Leu Leu Phe Ser
108 1 5 10 15
109 Gly Leu Trp His Leu Gly Leu Thr Ala Thr Asn Tyr Asn Cys Asp Asp
110 20 25 30
111 Pro Leu Ala Ser Leu Leu Ser Pro Met Ala Phe Ser Ser Ser Ser Asp
112 35 40 45
113 Leu Thr Gly Thr His Ser Pro Ala Gln Leu Asn Trp Arg Val Gly Thr
114 50 55 60
115 Gly Gly Trp Ser Pro Ala Asp Ser Asn Ala Gln Gln Trp Leu Gln Met
116 65 70 75 80
117 Asp Leu Gly Asn Arg Val Glu Ile Thr Ala Val Ala Thr Gln Gly Arg
118 85 90 95
119 Tyr Gly Ser Ser Asp Trp Val Thr Ser Tyr Ser Leu Met Phe Ser Asp
120 100 105 110
121 Thr Gly Arg Asn Trp Lys Gln Tyr Lys Gln Glu Asp Ser Ile Trp Thr
122 115 120 125
123 Phe Ala Gly Asn Met Asn Ala Asp Ser Val Val His His Lys Leu Leu
124 130 135 140
125 His Ser Val Arg Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn
126 145 150 155 160
127 Pro Ser Gly Lys Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr
128 165 170 175
129 Lys Ser Asp Val Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg
130 180 185 190
131 Phe Asn Gln Lys Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys
132 195 200 205
133 Phe Lys Ser Met Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln
134 210 215 220
135 Arg Gly Asp His Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu
136 225 230 235 240
137 His Leu Asn Leu Gly Asp Ser Lys Ala Arg Leu Ser Ser Ser Leu Pro
138 245 250 255
W--> 139 Ser Ala Thr Leu Gly Ser Leu Leu Asp Asp Gln His Trp His Xaa Val
140 260 265 270
141 Leu Ile Glu Arg Val Gly Lys Gln Val Asn Phe Thr Val Asp Lys His
142 275 280 285
143 Thr Gln His Phe Arg Thr Lys Gly Glu Thr Asp Ala Leu Asp Ile Asp
144 290 295 300
145 Tyr Glu Leu Ser Phe Gly Gly Ile Pro Val Pro Gly Lys Pro Gly Thr
146 305 310 315 320
147 Phe Leu Lys Lys Asn Phe His Gly Cys Ile Glu Asn Leu Tyr Tyr Asn
148 325 330 335
W--> 149 Gly Val Asn Ile Ile Xaa Leu Ala Lys Arg Arg Lys His Gln Ile Tyr
150 340 345 350
151 Thr Val Gly Asn Val Thr Phe Ser Cys Ser Glu Pro Gln Ile Val Pro
152 355 360 365
153 Ile Thr Phe Val Asn Ser Ser Gly Ser Tyr Leu Leu Leu Pro Gly Thr
154 370 375 380
155 Pro Gln Ile Asp Gly Leu Ser Val Ser Phe Gln Phe Arg Thr Trp Asn

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```

156 385          390          395          400
157 Lys Asp Gly Leu Leu Leu Ser Thr Glu Leu Ser Glu Gly Ser Gly Thr
158          405          410          415
159 Leu Leu Leu Ser Leu Glu Gly Gly Ile Leu Arg Leu Val Ile Gln Lys
160          420          425          430
161 Met Thr Glu Arg Val Ala Glu Ile Leu Thr Gly Ser Asn Leu Asn Asp
162          435          440          445
163 Gly Leu Trp His Ser Val Ser Ile Asn Ala Arg Arg Asn Arg Ile Thr
164          450          455          460
165 Leu Thr Leu Asp Asp Glu Ala Ala Pro Pro Ala Pro Asp Ser Thr Trp
166 465          470          475          480
167 Val Gln Ile Tyr Ser Gly Asn Ser Tyr Tyr Phe Gly Gly Cys Pro Asp
168          485          490          495
169 Asn Leu Thr Asp Ser Gln Cys Leu Asn Pro Ile Lys Ala Phe Gln Gly
170          500          505          510
171 Cys Met Arg Leu Ile Phe Ile Asp Asn Gln Pro Lys Asp Leu Ile Ser
172          515          520          525
173 Val Gln Gln Gly Ser Leu Gly Asn Phe Ser Asp Leu His Ile Asp Leu
174          530          535          540
175 Cys Ser Ile Lys Asp Arg Cys Leu Pro Asn Tyr Cys Glu His Gly Gly
176 545          550          555          560
177 Ser Cys Ser Gln Ser Trp Thr Thr Phe Tyr Cys Asn Cys Ser Asp Thr
178          565          570          575
179 Ser Tyr Thr Gly Ala Thr Cys His Asn Ser Ile Tyr Glu Gln Ser Cys
180          580          585          590
181 Glu Val Tyr Arg His Gln Gly Asn Thr Ala Gly Phe Phe Tyr Ile Asp
182          595          600          605
183 Ser Asp Gly Ser Gly Pro Leu Gly Pro Leu Gln Val Tyr Cys Asn Ile
184          610          615          620
185 Thr Glu Asp Lys Ile Trp Thr Ser Val Gln His Asn Asn Thr Glu Leu
186 625          630          635          640
187 Thr Arg Val Arg Gly Ala Asn Pro Glu Lys Pro Tyr Ala Met Ala Leu
188          645          650          655
189 Asp Tyr Gly Gly Ser Met Glu Gln Leu Glu Ala Val Ile Asp Gly Ser
190          660          665          670
191 Glu His Cys Glu Gln Glu Val Ala Tyr His Cys Arg Arg Ser Arg Leu
192          675          680          685
193 Leu Asn Thr Pro Asp Gly Thr Pro Phe Thr Trp Trp Ile Gly Arg Ser
194          690          695          700
195 Asn Glu Arg His Pro Tyr Trp Gly Gly Ser Pro Pro Gly Val Gln Gln
196 705          710          715          720
197 Cys Glu Cys Gly Leu Asp Glu Ser Cys Leu Asp Ile Gln His Phe Cys
198          725          730          735
199 Asn Cys Asp Ala Asp Lys Asp Glu Trp Thr Asn Asp Thr Gly Phe Leu
200          740          745          750
201 Ser Phe Lys Asp His Leu Pro Val Thr Gln Ile Val Ile Thr Asp Thr
202          755          760          765
203 Asp Arg Ser Asn Ser Glu Ala Ala Trp Arg Ile Gly Pro Leu Arg Cys
204          770          775          780

```

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```

205 Tyr Gly Asp Arg Arg Phe Trp Asn Ala Val Ser Phe Tyr Thr Glu Ala
206 785                      790                      795                      800
207 Ser Tyr Leu His Phe Pro Thr Phe His Ala Glu Phe Ser Ala Asp Ile
208                      805                      810                      815
209 Ser Phe Phe Phe Lys Thr Thr Ala Leu Ser Gly Val Phe Leu Glu Asn
210                      820                      825                      830
211 Leu Gly Ile Lys Asp Phe Ile Arg Leu Glu Ile Ser Ser Pro Ser Glu
212                      835                      840                      845
213 Ile Thr Phe Ala Ile Asp Val Gly Asn Gly Pro Val Glu Leu Val Val
214                      850                      855                      860
215 Gln Ser Pro Ser Leu Leu Asn Asp Asn Gln Trp His Tyr Val Arg Ala
216 865                      870                      875                      880
217 Glu Arg Asn Leu Lys Glu Thr Ser Leu Gln Val Asp Asn Leu Pro Arg
218                      885                      890                      895
219 Ser Thr Arg Glu Thr Ser Glu Glu Gly His Phe Arg Leu Gln Leu Asn
220                      900                      905                      910
221 Ser Gln Leu Phe Val Gly Gly Thr Ser Ser Arg Gln Lys Gly Phe Leu
222                      915                      920                      925
223 Gly Cys Ile Arg Ser Leu His Leu Asn Gly Gln Lys Met Asp Leu Glu
224                      930                      935                      940
225 Glu Arg Ala Lys Val Thr Ser Gly Val Arg Pro Gly Cys Pro Gly His
226 945                      950                      955                      960
227 Cys Ser Ser Tyr Gly Ser Ile Cys His Asn Gly Gly Lys Cys Val Glu
228                      965                      970                      975
229 Lys His Asn Gly Tyr Leu Cys Asp Cys Thr Asn Ser Pro Tyr Glu Gly
230                      980                      985                      990
231 Pro Phe Cys Lys Lys Glu Val Ser Ala Val Phe Glu Ala Gly Thr Ser
232                      995                      1000                      1005
233 Val Thr Tyr Met Phe Gln Glu Pro Tyr Pro Val Thr Lys Asn Ile Ser
234                      1010                      1015                      1020
235 Leu Ser Ser Ser Ala Ile Tyr Thr Asp Ser Ala Pro Ser Lys Glu Asn
236 1025                      1030                      1035                      1040
237 Ile Ala Leu Ser Phe Val Thr Thr Gln Ala Pro Ser Leu Leu Leu Phe
238                      1045                      1050                      1055
239 Ile Asn Ser Ser Ser Gln Asp Phe Val Val Val Leu Leu Cys Lys Asn
240                      1060                      1065                      1070
241 Gly Ser Leu Gln Val Arg Tyr His Leu Asn Lys Glu Glu Thr His Val
242                      1075                      1080                      1085
243 Phe Thr Ile Asp Ala Asp Asn Phe Ala Asn Arg Arg Met His His Leu
244                      1090                      1095                      1100
245 Lys Ile Asn Arg Glu Gly Arg Glu Leu Thr Ile Gln Met Asp Gln Gln
246 1105                      1110                      1115                      1120
247 Leu Arg Leu Ser Tyr Asn Phe Ser Pro Glu Val Glu Phe Arg Val Ile
248                      1125                      1130                      1135
249 Arg Ser Leu Thr Leu Gly Lys Val Thr Glu Asn Leu Gly Leu Asp Ser
250                      1140                      1145                      1150
251 Glu Val Ala Lys Ala Asn Ala Met Gly Phe Ala Gly Cys Met Ser Ser
252                      1155                      1160                      1165
253 Val Gln Tyr Asn His Ile Ala Pro Leu Lys Ala Ala Leu Arg His Ala

```

Use of n and / or Xaa has been detected in the  
Sequence Listing. Review the Sequence Listing  
to ensure a corresponding explanation is present  
in the <220> to <223> fields of each sequence  
using n or Xaa.

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/770,643A

DATE: 09/10/2001

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Input Set : A:\LEX-0122-USA SEQLIST.txt

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L:19 M:270 C: Current Application Number differs, Replaced Current Application No

L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:139 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2

L:149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2

L:385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4

L:657 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10

L:742 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:862 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14

L:987 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16

L:997 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16

L:1135 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18

L:1284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20

L:1294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20

L:1449 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22